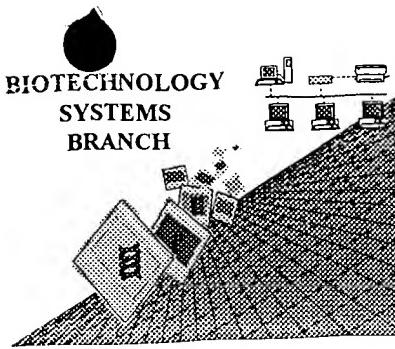


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/039,177B

RECEIVED

Source: 1647

MAR 01 2001

Date Processed by STIC: 2/14/2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/039,177B

DATE: 02/14/2001

TIME: 17:37:04

Does Not Comply
Corrected Diskette Needed

Input Set : A:\LUD-5539 SEQUENCE LISTING.txt

Output Set: N:\CRF3\02142001\I039177B.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Kohei MIYAZONO; Takeshi IMAMURA; Peter DEN DIJKE
7 (ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN, NUCLEIC ACIDS ENCODING
IT, AND USES THEREOF

10 (iii) NUMBER OF SEQUENCES: 46

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
14 (B) STREET: 666 Fifth Avenue
15 (C) CITY: New York City
16 (D) STATE: New York
17 (E) COUNTRY: USA
18 (F) ZIP: 10103

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
22 (B) COMPUTER: IBM PS/2
23 (C) OPERATING SYSTEM: PC-DOS
24 (D) SOFTWARE: Wordperfect

26 (vi) CURRENT APPLICATION DATA:

27 (A) APPLICATION NUMBER: US/09/039,177B

28 (B) FILING DATE: 13-Mar-1998

29 (C) CLASSIFICATION: 435

59 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: PCT/GB93/02367

33 (B) FILING DATE: November 17, 1993

36 (A) APPLICATION NUMBER: GB 9224057.1

37 (B) FILING DATE: November 17, 1992

40 (A) APPLICATION NUMBER: GB 9304677.9

41 (B) FILING DATE: March 8, 1993

44 (A) APPLICATION NUMBER: GB 9304680.3

45 (B) FILING DATE: March 8, 1993

48 (A) APPLICATION NUMBER: 9311047.6

49 (B) FILING DATE: May 28, 1993

52 (A) APPLICATION NUMBER: 9313763.6

53 (B) FILING DATE: July 2, 1993

56 (A) APPLICATION NUMBER: 9136099.2

57 (B) FILING DATE: August 3, 1993

60 (A) APPLICATION NUMBER: 321344.5

61 (B) FILING DATE: October 15, 1993

63 (viii) ATTORNEY/AGENT INFORMATION:

64 (A) NAME: Mary Anne Schofield

65 (B) REGISTRATION NUMBER: 36,669

66 (C) REFERENCE/DOCKET NUMBER: LUD 5539 CIP - JEL/MAS

68 (ix) TELECOMMUNICATION INFORMATION:

69 (A) TELEPHONE: (202) 662-0200

70 (B) TELEFAX: (202) 662-4643

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177B

DATE: 02/14/2001
TIME: 17:37:04

Input Set : A:\LUD-5539 SEQUENCE LISTING.txt
Output Set: N:\CRF3\02142001\I039177B.raw

ERRORED SEQUENCES

2641 (2) INFORMATION FOR SEQ ID NO: 32:
 2642 (i) SEQUENCE CHARACTERISTICS:
 2643 (A) LENGTH: 175 amino acids
 2644 (B) TYPE: amino acid
 2645 (D) TOPOLOGY: linear
 2647 (ii) MOLECULE TYPE: peptide
 2649 (vi) ORIGINAL SOURCE:
 2650 (A) ORGANISM: Mouse
 2652 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
 2654 Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys Ala
 2655 5 10 15
 2656 Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln Asp
 2657 20 25 30
 2658 Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly Met
 2659 35 40 45
 2660 Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly Thr
 2661 50 55 60
 2662 Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys Gly
 2663 65 70 75 80
 2664 Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu Leu
 2665 85 90 95
 2666 Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His Glu
 2667 100 105 110
 2668 Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His Arg
 2669 115 120 125
 2670 Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala Cys
 2671 130 135 140
 2672 Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser Ala
 2673 145 150 155 160
 2674 Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
 E--> 2675 165 170 175 165 170
 2717 (2) INFORMATION FOR SEQ ID NO: 34:
 2718 (i) SEQUENCE CHARACTERISTICS:
 2719 (A) LENGTH: 513 amino acids
 2720 (B) TYPE: amino acid
 2721 (D) TOPOLOGY: linear
 2723 (ii) MOLECULE TYPE: peptide
 2725 (vi) ORIGINAL SOURCE:
 2726 (A) ORGANISM: MOUSE
 2728 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
 2730 ~~SEQ ID NO: 34~~ (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
 E--> 2731 ~~Mouse ActR II~~ delete this
 E--> 2733 Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
 2734 5 10 15
 2735 Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
 2736 20 25 30
 2737 Phe Asn Ala Asn Trp Glu lys Asp Arg Thr Asn Gln Thr Gly Val Glu
 2738 35 40 45

(see item 4 on
Error Summary Sheet)

misaligned amino
acid numbering

165 170

RAW SEQUENCE LISTING

DATE: 02/14/2001

PATENT APPLICATION: US/09/039,177B

TIME: 17:37:04

Input Set : A:\LUD-5539 SEQUENCE LISTING.txt

Output Set: N:\CRF3\02142001\I039177B.raw

2739 Pro Cys Tyr Gly Asp Lys Arg Arg His Cys Phe Ala Thr Trp
 2740 50 55 60
 2741 Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
 2742 65 70 75 80
 2743 Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp
 2744 85 90 95
 2745 Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
 2746 100 105 110
 2747 Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn
 2748 115 120 125
 2749 Pro Val Thr Pro Lys Pro Pro Tyr Tyr Asn Ile Leu Leu Tyr Ser Leu
 2750 130 135 140
 2751 Val Pro Leu Met Leu Ile Ala Gly Ile Val Ile Cys Ala Phe Trp Val
 2752 145 150 155 160
 2753 Tyr Arg His His Lys Met Ala Tyr Pro Pro Val Leu Val Pro Thr Gln
 2754 165 170 175
 2755 Asp Pro Gly Pro Pro Pro Ser Pro Leu Leu Gly Leu Lys Pro Leu
 2756 180 185 190
 2757 Gln Leu Leu Glu Val Lys Ala Arg Gly Arg Phe Gly Cys Val Trp Lys
 2758 195 200 205
 2759 Ala Gln Leu Leu Asn Glu Tyr Val Ala Val Lys Ile Phe Pro Ile Gln
 2760 210 215 220
 2761 Asp Lys Gln Ser Trp Gln Asn Glu Tyr Glu Val Tyr Ser Leu Pro Gly
 2762 225 230 235 240
 2763 Met Lys His Glu Asn Ile Leu Gln Phe Ile Gly Ala Glu Lys Arg Gly
 2764 245 250 255
 2765 Thr Ser Val Asp Val Asp Leu Trp Leu Ile Thr Ala Phe His Glu Lys
 2766 260 265 270
 2767 Gly Ser Leu Ser Asp Phe Leu Lys Ala Asn Val Val Ser Trp Asn Glu
 2768 275 280 285
 2769 Leu Cys His Ile Ala Glu Thr Met Ala Arg Gly Leu Ala Tyr Leu His
 2770 290 295 300
 2771 Glu Asp Ile Pro Gly Leu Lys Asp Gly His Lys Pro Ala Ile Ser His
 2772 305 310 315 320
 2773 Arg Asp Ile Lys Ser Lys Asn Val Leu Leu Lys Asn Asn Leu Thr Ala
 2774 325 330 335
 2775 Cys Ile Ala Asp Phe Gly Leu Ala Leu Lys Phe Glu Ala Gly Lys Ser
 2776 340 345 350
 2777 Ala Gly Asp Thr His Gly Gln Val Gly Thr Arg Arg Tyr Met Ala Pro
 2778 355 360 365
 2779 Glu Val Leu Glu Gly Ala Ile Asn Phe Gln Arg Asp Ala Phe Leu Arg
 2780 370 375 380
 2781 Ile Asp Met Tyr Ala Met Gly Leu Val Leu Trp Glu Leu Ala Ser Arg
 2782 385 390 395 400
 2783 Cys Thr Ala Ala Asp Gly Pro Val Asp Glu Tyr Met Leu Pro Phe Glu
 2784 405 410 415
 2785 Glu Glu Ile Gly Gln His Pro Ser Leu Glu Asp Met Gln Glu Val Val
 2786 420 425 430
 2787 Val His Lys Lys Lys Arg Pro Val Leu Arg Asp Tyr Trp Gln Lys His

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/039,177B

DATE: 02/14/2001

TIME: 17:37:04

Input Set : A:\LUD-5539 SEQUENCE LISTING.txt
 Output Set: N:\CRF3\02142001\I039177B.raw

2788 435 440 445
 2789 Ala Gly Met Ala Met Leu Cys Glu Thr Ile Glu Glu Cys Trp Asp His
 2790 450 455 460
 2791 Asp Ala Glu Ala Arg Leu Ser Ala Gly Cys Val Gly Glu Arg Ile Thr
 2792 465 470 475 480
 2793 Gln Met Gln Arg Leu Thr Asn Ile Ile Thr Thr Glu Asp Ile Val Thr
 2794 485 490 495
 2795 Val Val Thr Met Val Thr Asn Val Asp Phe Pro Pro Lys Glu Ser Ser
 2796 500 505 510

~~OK~~ > 2797 Leu

2800 (2) INFORMATION FOR SEQ ID NO: 35:
 2801 (i) SEQUENCE CHARACTERISTICS:
 2802 (A) LENGTH: 536 amino acids
 2803 (B) TYPE: amino acid
 2804 (D) TOPOLOGY: linear
 2806 (ii) MOLECULE TYPE: peptide
 2808 (vi) ORIGINAL SOURCE:
 2809 (A) ORGANISM: MOUSE
 2811 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

E--> 2813 ~~ACTR- IIB~~ *delete*

E--> 2815 Met Thr Ala Pro Trp Ala Ala Leu Ala Leu Leu Trp Gly Ser Leu Cys
 2816 5. 10 15
 2818 Ala Gly Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu Cys Ile Tyr Tyr
 2819 20 25 30
 2820 Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser Gly Leu Glu Arg
 2821 35 40 45
 2822 Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr Ala Ser Trp Arg
 2823 50 55 60
 2824 Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly Cys Trp Leu Asp
 2825 65 70 75 80
 2826 Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala Thr Glu Glu Asn
 2827 85 90 95
 2828 Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe Cys Asn Glu Arg
 2829 100 105 110
 2830 Phe Thr His Leu Pro Glu Pro Gly Gly Pro Glu Val Thr Tyr Glu Pro
 2831 115 120 125
 2832 Pro Pro Thr Ala Pro Thr Leu Leu Thr Val Leu Ala Tyr Ser Leu Leu
 2833 130 135 140
 2834 Pro Ile Gly Gly Leu Ser Leu Ile Val Leu Leu Ala Phe Trp Met Tyr
 2835 145 150 155 160
 2836 Arg His Arg Lys Pro Pro Tyr Gly His Val Asp Ile His Glu Val Arg
 2837 165 170 175
 2838 Gln Cys Gln Arg Trp Ala Gly Arg Arg Asp Gly Cys Ala Asp Ser Phe
 2839 180 185 190
 2840 Lys Pro Leu Pro Phe Gln Asp Pro Gly Pro Pro Pro Pro Ser Pro Leu
 2841 195 200 205
 2842 Val Gly Leu Lys Pro Leu Gln Leu Leu Glu Ile Lys Ala Arg Gly Arg
 2843 210 215 220
 2844 Phe Gly Cys Val Trp Lys Ala Gln Leu Met Asn Asp Phe Val Ala Val

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177B

DATE: 02/14/2001
TIME: 17:37:04

Input Set : A:\LUD-5539 SEQUENCE LISTING.txt
Output Set: N:\CRF3\02142001\I039177B.raw

2845	225	230	235	240
2846	Lys Ile Phe Pro Leu Gln Asp Lys Gln Ser Trp Gln Ser Glu Arg Glu			
2847	245	250	255	
2848	Ile Phe Ser Thr Pro Gly Met Lys His Glu Asn Leu Leu Gln Phe Ile			
2849	260	265	270	
2850	Ala Ala Glu Lys Arg Gly Ser Asn Leu Glu Val Glu Leu Trp Leu Ile			
2851	275	280	285	
2852	Thr Ala Phe His Asp Lys Gly Ser Leu Thr Asp Tyr Leu Lys Gly Asn			
2853	290	295	300	
2854	Ile Ile Thr Trp Asn Glu Leu Cys His Val Ala Glu Thr Met Ser Arg			
2855	305	310	315	320
2856	Gly Leu Ser Tyr Leu His Glu Asp Val Pro Trp Cys Arg Gly Glu Gly			
2857	325	330	335	
2858	His Lys Pro Ser Ile Ala His Arg Asp Phe Lys Ser Lys Asn Val Leu			
2859	340	345	350	
2860	Leu Lys Ser Asp Leu Thr Ala Val Leu Ala Asp Phe Gly Leu Ala Val			
2861	355	360	365	
2862	Arg Phe Glu Pro Gly Lys Pro Pro Gly Asp Thr His Gly Gln Val Gly			
2863	370	375	380	
2864	Thr Arg Arg Tyr Met Ala Pro Glu Val Leu Glu Gly Ala Ile Asn Phe			
2865	385	390	395	400
2866	Gln Arg Asp Ala Phe Leu Arg Ile Asp Met Tyr Ala Met Gly Leu Val			
2867	405	410	415	
2868	Leu Trp Glu Leu Val Ser Arg Cys Lys Ala Ala Asp Gly Pro Val Asp			
2869	420	425	430	
2870	Glu Tyr Met Leu Pro Phe Glu Glu Glu Ile Gly Gln His Pro Ser Leu			
2871	435	440	445	
2872	Glu Glu Leu Gln Glu Val Val Val His Lys Lys Met Arg Pro Thr Ile			
2873	450	455	460	
2874	Lys Asp His Trp Leu Lys His Pro Gly Leu Ala Gln Leu Cys Val Thr			
2875	465	470	475	480
2876	Ile Glu Glu Cys Trp Asp His Asp Ala Glu Ala Arg Leu Ser Ala Gly			
2877	485	490	495	
2878	Cys Val Glu Glu Arg Val Ser Leu Ile Arg Arg Ser Val Asn Gly Thr			
2879	500	505	510	
2880	Thr Ser Asp Cys Leu Val Ser Leu Val Thr Ser Val Thr Asn Val Asp			
E--> 2881	515	520	525	535
2882	Leu Leu Pro Lys Glu Ser Ser Ile			
E--> 2883	530	535	535	
3075	(2) INFORMATION FOR SEQ ID NO: 38:			
3076	(i) SEQUENCE CHARACTERISTICS:			
3077	(A) LENGTH: 6 amino acids			
3078	(B) TYPE: amino acid			
3079	(D) TOPOLOGY: linear			
3081	(ii) MOLECULE TYPE: peptide			
3083	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:			
3085	Asp Leu Lys Pro Glu Asn			
E--> 3086	5 - misaligned nos.			
3092	(2) INFORMATION FOR SEQ ID NO: 39:			

misaligned nos.

520

525

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177B

DATE: 02/14/2001
TIME: 17:37:04

Input Set : A:\LUD-5539 SEQUENCE LISTING.txt
Output Set: N:\CRF3\02142001\I039177B.raw

3093 (i) SEQUENCE CHARACTERISTICS:
3094 (A) LENGTH: 6 amino acids
3095 (B) TYPE: amino acid
3096 (D) TOPOLOGY: linear
3098 (ii) MOLECULE TYPE: peptide
3100 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:
3102 Asp Leu Ala Ala Arg Asn

E--> 3103 S -
3106 (2) INFORMATION FOR SEQ ID NO: 40:
3107 (i) SEQUENCE CHARACTERISTICS:
3108 (A) LENGTH: 6 amino acids
3109 (B) TYPE: amino acid
3110 (D) TOPOLOGY: linear
3112 (ii) MOLECULE TYPE: peptide
3114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:
3116 Asp Ile Lys Ser Lys Asn

E--> 3117 S -
3120 (2) INFORMATION FOR SEQ ID NO: 41:
3121 (i) SEQUENCE CHARACTERISTICS:
3122 (A) LENGTH: 6 amino acids
3123 (B) TYPE: amino acid
3124 (D) TOPOLOGY: linear
3126 (ii) MOLECULE TYPE: peptide
3128 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:
3130 Asp Phe Lys Ser Lys Asn

E--> 3131 S -
3134 (2) INFORMATION FOR SEQ ID NO: 42:
3135 (i) SEQUENCE CHARACTERISTICS:
3136 (A) LENGTH: 6 amino acids
3137 (B) TYPE: amino acid
3138 (D) TOPOLOGY: linear
3140 (ii) MOLECULE TYPE: peptide
3142 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:
3144 Asp Leu Lys Ser Ser Asn

E--> 3145 S -
3148 (2) INFORMATION FOR SEQ ID NO: 43:
3149 (i) SEQUENCE CHARACTERISTICS:
3150 (A) LENGTH: 6 amino acids
3151 (B) TYPE: amino acid
3152 (D) TOPOLOGY: linear
3154 (ii) MOLECULE TYPE: peptide
3156 (ix) FEATURE:
3157 (D) OTHER INFORMATION: First Xaa is Thr or Ser;
3158 fourth Xaa is Tyr or Phe; Each other Xaa
3159 may be any amino acid
3161 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:
W--> 3163 Gly Xaa Xaa Xaa Xaa Xaa
E--> 3164 S -
3167 (2) INFORMATION FOR SEQ ID NO: 44:

misaligned nos.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/039,177B

DATE: 02/14/2001
TIME: 17:37:04

Input Set : A:\LUD-5539 SEQUENCE LISTING.txt
Output Set: N:\CRF3\02142001\I039177B.raw

3168 (i) SEQUENCE CHARACTERISTICS:
3169 (A) LENGTH: 6 amino acids
3170 (B) TYPE: amino acid
3171 (D) TOPOLOGY: linear
3173 (ii) MOLECULE TYPE: peptide *First*
3175 (ix) FEATURE:
3176 (D) OTHER INFORMATION: *Fisrt* Xaa is any amino acid;
3177 second Xaa is Ile or Val;
3178 third Xaa is Lys or Arg;
3179 fourth Xaa is Thr or Met.
3181 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:
W--> 3183 Xaa Pro Xaa Xaa Trp Xaa
E--> 3184 *5*
3187 (2) INFORMATION FOR SEQ ID NO: 45:
3188 (i) SEQUENCE CHARACTERISTICS:
3189 (A) LENGTH: 6 amino acids
3190 (B) TYPE: amino acid
3191 (D) TOPOLOGY: linear
3193 (ii) MOLECULE TYPE: peptide
3195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:
3197 Gly Thr Arg Arg Tyr Met
E--> 3198 *5*
3200 (2) INFORMATION FOR SEQ ID NO: 46:
3201 (i) SEQUENCE CHARACTERISTICS:
3202 (A) LENGTH: amino acids *mandatory response needed*
3203 (B) TYPE: amino acid
3204 (D) TOPOLOGY: linear
3206 (ii) MOLECULE TYPE: peptide
3208 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:
3210 Gly Thr Ala Arg Tyr Met
E--> 3211 *5* *misaligned nos.*

All next page - more errors

09/039,177B 8

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 669 amino acids
 - (B) TY7PE amino acid → TYPE
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: C. elegans

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

SEQ ID NO: 37
C. elegans Daf-1:

delete

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/039,177B

DATE: 02/14/2001
TIME: 17:37:05

Input Set : A:\LUD-5539 SEQUENCE LISTING.txt
Output Set: N:\CRF3\02142001\I039177B.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:85 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:331 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:602 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:887 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1143 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1398 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1640 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:1897 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2148 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2391 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2409 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2427 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2445 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2463 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2481 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2499 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:2518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:2675 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:32
L:0 M:200 E: Mandatory Header Field missing, Seq 34, [(B) TYPE:] of (2)(i)
L:2731 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:2731 M:330 E: (2) Invalid Amino Acid Designator, 2
L:2733 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
L:2797 M:203 E: No. of Seq. differs, LENGTH:Input:513 Found:515 SEQ:34
L:2813 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:2813 M:330 E: (2) Invalid Amino Acid Designator, 2
L:2815 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
M:332 Repeated in SeqNo=35
L:2883 M:203 E: No. of Seq. differs, LENGTH:Input:536 Found:538 SEQ:35
L:0 M:200 E: Mandatory Header Field missing, Seq 37, [(B) TYPE:] of (2)(i)
L:3086 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:38
L:3103 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:39
L:3117 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:40
L:3131 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:41
L:3145 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
L:3163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:3164 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
L:3183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:3184 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
L:3198 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
L:3211 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
L:3211 M:203 E: No. of Seq. differs, LENGTH:Input:0 Found:6 SEQ:46

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/039,177B</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	RECEIVED
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	MAR 01 2001
4 <input checked="" type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	TECH CENTER 1600/2900
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) _____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	